

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Luyten, Frank P.
Hoang, Bang
Moos, Jr., Malcolm
Wang, Shouwen

(ii) TITLE OF THE INVENTION: METHOD OF MODULATING TISSUE GROWTH USING
'RZB PROTEIN

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
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(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bartfeld, Neil S
(B) REGISTRATION NUMBER: 39,901
(C) REFERENCE/DOCKET NUMBER: NIH133.001CP1

(ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: 619-235-0176
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10028051.121901

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 256...1230
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATAGATGCC	GCGGCCCCAG	AAGTCTTAGA	CGTCGGGAAA	GAGCAGCCGG	AGAGGCAGGG	60
GCGGCGGCGG	CTGGCGCTCG	GCGCAGCTTT	TGGGACCCCA	TTGAGGGAAT	TTGATCCAAG	120
GAAGCTGTGA	GATTGCCGGG	GGAGGAGAAG	CTCCCATATC	ATTGTGTCCA	CTTCCAGGGC	180
GGGAGGAGG	AAACGGCGGA	GCGGGCCTCT	CGGCGTTCTC	CGCACTGCTG	CACCCTGCCC	240
CATCCTGCCG	AGATC	ATG GTC	TGC GGG	AGC CGA	GGC GGG	291
	Met	Val	Cys	Gly	Ser Arg Gly Gly Met Leu Leu Leu	
	1			5		10

CCG GCC GGG CTA CTC GCC CTG GCT GCG CTC TGC CTG CTC CGC GTG CCC	339
Pro Ala Gly Leu Leu Ala Leu Ala Leu Cys Leu Leu Arg Val Pro	---
15 20 25	

GGA GCG CGG GCG GCC GCC TGT GAG CCC GTT CGC ATT CCC CTG TGC AAG	387
Gly Ala Arg Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys	
30 35 40	

TCC CTG CCC TGG AAC ATG ACT AAG ATG CCC AAC CAC CTG CAC CAC AGC	435
Ser Leu Pro Trp Asn Met Thr Lys Met Pro Asn His Leu His His Ser	
45 50 55 60	

ACC CAG GCC AAC GCC ATC CTG GCC ATC GAG CAG TTC GAA GGT CTG CTG	483
Thr Gln Ala Asn Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu	
65 70 75	

GGC ACC CAC TGC AGC CCG GAT CTG CTC TTC TTC CTC TGT GCT ATG TAC	531
Gly Thr His Cys Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr	
80 85 90	

GCG CCC ATC TGC ACC ATT GAC TTC CAG CAC GAG CCC ATC AAG CCC TGC	579
Ala Pro Ile Cys Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys	
95 100 105	

AAG TCT GTG TGC GAG CGG GCC CGG CAG GGC TGT GAG CCC ATC CTC ATC	627
Lys Ser Val Cys Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile	
110 115 120	

AAG TAC CGC CAC TCG TGG CCG GAA AGC CTG GCC TGC GAG GAG CTG CCA	675
Lys Tyr Arg His Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro	
125 130 135 140	

GTA TAT GAC CGC GGC GTG TGC ATC TCT CCG GAG GCC ATC GTC ACT GCC	723
Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala	
145 150 155	

GAC GGA GCC GAT TTT CCT ATG GAT TCC AGT AAT GGA AAC TGT AGA GGA	771
Asp Gly Ala Asp Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly	
160 165 170	

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GTGCACTGGC CTGCACTTTA TCATTGGAT TTGTGCTGTT TAATGCTCAG TAAATATGC 2337
TTAATAAAAG GAAAAA AAAA AAAAAA 2374

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu Pro Ala Gly Leu
1 10 15
Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Glu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn Leu Tyr Thr Ser
225 230 235 240
Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Leu Ile
245 250 255
Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270
Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 280 285
Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr Ser Asp Ser Ser
290 295 300
His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser
305 310 315 320
Arg Gln Ala Arg Asn

10028051.121901

325

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 208...1182
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGGGCTTGG GCGGSAGGGG CGGTGGCTGG AGCTCGGTAA AGCTCGTGG ACCCCATTGG 60
GGGAATTGA TCCAAGGAAG CGGTGATTGC CGGGGGAGGA GAAGCTCCCA GATCCTTGTG 120
TCCACTTGCA GCGGGGGAGG CGGAGACGCG GAGCGGGCCCT TTTGGCGTCC ACTGCGCGGC 180
TGCACCCTGC CCCATCCTGC CGGGATC ATG GTC TGC GGC AGC CCG GGA GGG ATG 234
Met Val Cys Gly Ser Pro Gly Gly Met
1 5

CTG CTG CTG CGG GCC GGG CTG CTT GCC CTG GCT GCT CTC TGC CTG CTC 282
Leu Leu Leu Arg Ala Gly Leu Leu Ala Leu Ala Leu Cys Leu Leu 25

CGG GTG CCC GGG GCT CGG GCT GCA GCC TGT GAG CCC GTC CGC ATC CCC 330
Arg Val Pro Gly Ala Arg Ala Ala Cys Glu Pro Val Arg Ile Pro 40

CTG TGC AAG TCC CTG CCC TGG AAC ATG ACT AAG ATG CCC AAC CAC CTG 378
Leu Cys Lys Ser Leu Pro Trp Asn Met Thr Lys Met Pro Asn His Leu 55

CAC CAC AGC ACT CAG GCC AAC GCC ATC CTG GCC ATC GAG CAG TTC GAA 426
His His Ser Thr Gln Ala Asn Ala Ile Leu Ala Ile Glu Gln Phe Glu 65 70

GGT CTG CTG GGC ACC CAC TGC AGC CCC GAT CTG CTC TTC TTC CTC TGT 474
Gly Leu Leu Gly Thr His Cys Ser Pro Asp Leu Leu Phe Phe Leu Cys 80 85

GCC ATG TAC GCG CCC ATC TGC ACC ATT GAC TTC CAG CAC GAG CCC ATC 522
Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe Gln His Glu Pro Ile 90 95 100 105

AAG CCC TGT AAG TCT GTG TGC GAG CGG GCC CGG CAG GGC TGT GAG CCC 570
Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg Gln Gly Cys Glu Pro 110 115 120

ATA CTC ATC AAG TAC CGC CAC TCG TGG CCG GAG AAC CTG GCC TGC GAG 618
Ile Leu Ile Lys Tyr Arg His Ser Trp Pro Glu Asn Leu Ala Cys Glu 125 130 135

GAG Glu	CTG Leu	CCA Pro 140	GTG Val	TAC Tyr	GAC Asp	AGG Arg	GGC Gly 145	GTG Val	TGC Cys	ATC Ile	TCT Ser	CCC Pro 150	GAG Glu	GCC Ala	ATC Ile	666
GTT Val	ACT Thr 155	GCG Ala	GAC Asp	GGA Gly	GCT Ala	GAT Asp 160	TTT Phe	CCT Pro	ATG Met	GAT Asp	TCT Ser 165	AGT Ser	AAC Asn	GGA Gly	AAC Asn	714
TGT Cys 170	AGA Arg	GGG Gly	GCA Ala	AGC Ser	AGT Ser 175	GAA Glu	CGC Arg	TGT Cys	AAA Lys 180	TGT Cys	AAG Lys	CCT Pro	ATT Ile	AGA Arg	GCT Ala 185	762
ACA Thr	CAG Gln	AAG Lys	ACC Thr	TAT Tyr 190	TTC Phe	CGG Arg	AAC Asn	AAT Asn	TAC Tyr 195	AAC Asn	TAT Tyr	GTC Val	ATT Ile	CGG Arg 200	GCT Ala	810
AAA Lys	GTT Val	AAA Lys	GAG Glu 205	ATA Ile	AAG Lys	ACT Thr	AAG Lys	TGC Cys 210	CAT His	GAT Asp	GTG Val	ACT Thr	GCA Ala 215	GTA Val	GTG Val	858
GAG Glu	GTG Val	AAG Lys 220	GAG Glu	ATT Ile	CTA Leu	AAG Lys	TCC Ser 225	TCT Ser	CTG Leu	GTA Val	AAC Asn	ATT Ile 230	CCA Pro	CGG Arg	GAC Asp	906
ACT Thr	GTC Val 235	AAC Asn	CTC Leu	TAT Tyr	ACC Thr	AGC Ser 240	TCT Ser	GGC Gly	TGC Cys	CTC Leu	TGC Cys 245	CCT Pro	CCA Pro	CTT Leu	AAT Asn	954
GTT Val 250	AAT Asn	GAG Glu	GAA Glu	TAT Tyr	ATC Ile 255	ATC Met	GGC Gly	TAT Tyr	GAA Glu 260	GAT Glu	GAG Glu	GAA Glu	CGT Arg	TCC Ser 265		1002
AGA Arg	TTA Leu	CTC Leu	TTG Leu	GTG Val 270	GAA Glu	GGC Gly	TCT Ser	ATA Ile	GCT Ala 275	GAG Glu	AAG Lys	TGG Trp	AAG Lys	GAT Asp 280	CGA Arg	1050
CTC Leu	GGT Gly	AAA Lys 285	AAA Lys	GTT Val	AAG Lys	CGC Arg	TGG Trp	GAT Asp 290	ATG Met	AAG Lys	CTT Leu	CGT Arg	CAT His 295	CTT Leu	GGA Gly	1098
CTC Leu	AGT Ser	AAA Lys 300	AGT Ser	GAT Asp	TCT Ser	AGC Ser	AAT Asn 305	AGT Ser	GAT Asp	TCC Ser	ACT Thr	CAG Gln 310	AGT Ser	CAG Gln	AAG Lys	1146
TCT Ser	GGC Gly 315	AGG Arg	AAC Asn	TCG Ser	AAC Asn	CCC Pro 320	CGG Arg	CAA Gln	GCA Ala	CGC Arg	AAC Asn 325	TAAATCCCGA AATACA			1198	
AAAAGTAACA CAGTGGACTT CCTATTAAGA CTTACTTGCA TTGCTGGACT AGCAAAGGAA																1258
AATTGCACTA TTGCACATCA TATTTCTATTG TTTACTATAA AAATCATGTG ATAACCTGATT																1318
ATTACTTCTG TTTCTCTTTT GGTTCCTGCT TCTCTCTTCT CTCACCCCTT TTGTAATGGT																1378
TTGGGGGCGC ACTCTTAAAT ATATTGTGAG TTTTCTATT CACTAATCAT GAGAAAAACT																1438
GTTCTTTTGC AATAATAATA AATTAAACAT GCTGTAAAA AAAAAA																1484

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Cys Gly Ser 5 Pro Gly Gly Met 10 Leu Leu Arg Ala Gly Leu
1 Leu Ala Leu Ala Ala 20 Leu Cys Leu Leu 25 Arg Val Pro Gly Ala Arg Ala
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser 30 Leu Pro Trp
35 Asn Met Thr Lys Met Pro Asn His Leu His His Ser 45 Thr Gln Ala Asn
50 Ala Ile Leu Ala Ile 55 Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
165 Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
195 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
225 Ser Gly Cys Leu Cys 230 Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
245 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
290 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
305 Arg Gln Ala Arg Asn 310 315 320
325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys	Gln	Pro	Ile	Ser	Ile	Pro	Leu	Cys	Thr	Asp	Ile	Ala	Tyr	Asn	Gln	
1				5					10					15		
Thr	Ile	Met	Pro	Asn	Leu	Leu	Gly	His	Thr	Asn	Gln	Glu	Asp	Ala	Gly	
			20					25					30			
Leu	Glu	Val	His	Gln	Phe	Tyr	Pro	Leu	Val	Lys	Val	Gln	Cys	Ser	Ala	
		35					40				45					
Glu	Leu	Lys	Phe	Phe	Leu	Cys	Ser	Met	Tyr	Ala	Pro	Val	Cys	Thr	Val	
	50					55					60					
Leu	Glu	Gln	Ala	Leu	Pro	Cys	Arg	Ser	Leu	Cys	Glu	Arg	Ala	Gln		
65					70				75					80		
Gly	Cys	Glu	Ala	Leu	Met	Asn	Lys	Phe	Gly	Phe	Gln	Trp	Pro	Asp	Thr	---
				85					90					95		
Leu	Lys	Cys	Glu	Lys	Phe	Pro	Val	His	Gly	Arg	Gly	Glu	Leu	Cys		
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Glu	Pro	Ile	Thr	Ile	Ser	Ile	Cys	Lys	Asn	Ile	Pro	Tyr	Asn	Met	
1				5					10					15		
Thr	Ile	Met	Pro	Asn	Leu	Ile	Gly	His	Thr	Lys	Gln	Glu	Glu	Ala	Gly	
			20					25					30			
Leu	Glu	Val	His	Gln	Phe	Ala	Pro	Leu	Val	Lys	Ile	Gly	Cys	Ser	Asp	
		35					40				45					
Asp	Leu	Gln	Leu	Phe	Leu	Cys	Ser	Leu	Tyr	Val	Pro	Val	Cys	Thr	Ile	
	50					55					60					
Leu	Glu	Arg	Pro	Ile	Pro	Pro	Cys	Arg	Ser	Leu	Cys	Glu	Ser	Ala	Arg	
65					70				75					80		
Val	Cys	Glu	Lys	Leu	Met	Lys	Thr	Tyr	Asn	Phe	Asn	Trp	Pro	Glu	Asn	
				85					90					95		
Leu	Glu	Cys	Ser	Lys	Phe	Pro	Val	His	Gly	Gly	Glu	Asp	Leu	Cys		
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Pro	Thr	Arg	Lys	Leu	Asp	Ser	Phe	Leu	Leu	Leu	Val	Ile	Pro
1				5					10					15	
Gly	Leu	Val	Leu	Leu	Leu	Leu	Pro	Asn	Ala	Tyr	Cys	Ala	Ser	Cys	Glu
			20					25					30		
Pro	Val	Arg	Ile	Pro	Met	Cys	Lys	Ser	Met	Pro	Trp	Asn	Met	Thr	Lys
		35				40						45			
Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala
	50				55					60					
Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Thr	Thr	Glu	Cys	Ser	Gln	Asp	Leu
65				70					75					80	
Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe
			85						90					95	
Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala	Arg
			100					105					110		
Ala	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	Ile	Trp	Pro	Glu
		115				120						125			
Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys	Ile
	130					135					140				
Ser	Pro	Glu	Ala	Ile	Val	Thr	Val	Glu	Gln	Gly	Thr	Asp	Ser	Met	Pro
145				150					155					160	
Asp	Phe	Pro	Met	Asp	Ser	Asn	Asn	Gly	Asn	Cys	Gly	Ser	Thr	Ala	Gly
			165					170						175	
Glu	His	Cys	Lys	Cys	Lys	Pro	Met	Lys	Ala	Ser	Gln	Lys	Thr	Thr	Leu
			180					185				190			
Lys	Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Val	Lys
	195					200						205			
Val	Lys	Cys	His	Asp	Ala	Thr	Ala	Ile	Val	Glu	Val	Lys	Glu	Ile	Leu
	210					215					220				
Lys	Ser	Ser	Leu	Val	Asn	Ile	Pro	Lys	Asp	Thr	Val	Ile	Leu	Tyr	Thr
225					230					235				240	
Asn	Ser	Gly	Cys	Leu	Cys	Pro	Gln	Leu	Val	Ala	Asn	Glu	Glu	Tyr	Ile
			245					250						255	
Ile	Met	Gly	Tyr	Glu	Asp	Lys	Glu	Arg	Thr	Arg	Leu	Leu	Leu	Val	Glu
		260						265					270		
Gly	Ser	Leu	Ala	Glu	Lys	Trp	Arg	Asp	Arg	Leu	Ala	Lys	Lys	Val	Lys
	275						280					285			
Arg	Trp	Asp	Gln	Lys	Leu	Arg	Arg	Pro	Arg	Lys	Ser	Lys	Asp	Pro	Val
	290					295					300				
Ala	Pro	Ile	Pro	Asn	Lys	Asn	Ser	Asn	Ser	Arg	Gln	Ala	Arg	Ser	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Val	Cys	Gly	Ser	Gly	Gly	Met	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Ala
1				5				10					15		

Leu	Ala	Ala	Leu	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg	Ala	Ala	Cys	
			20					25					30		
Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	Asn	Met	Thr
			35				40					45			
Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu
			50			55					60				
Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	Ser	Pro	Asp
65					70					75				80	
Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp
				85					90					95	
Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala
			100					105					110		
Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	Ser	Trp	Pro
			115				120					125			
Glu	Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys
			130				135				140				
Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	Phe	Pro	Met
145					150					155				160	
Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser	Glu	Arg	Cys	Lys
				165					170					175	
Cys	Lys	Pro	Arg	Ala	Ile	Gln	Lys	Thr	Tyr	Phe	Arg	Asn	Asn	Tyr	Asn
			180					185				190			
Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Ile	Lys	Ile	Lys	Cys	His	Asp
			195				200					205			
Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys	Ser	Ser	Leu	Val
			210				215				220				
Asn	Ile	Pro	Arg	Asp	Thr	Val	Asn	Leu	Tyr	Thr	Ser	Ser	Gly	Cys	Leu
225					230					235				240	
Cys	Pro	Pro	Leu	Asn	Val	Asn	Glu	Glu	Tyr	Ile	Ile	Met	Gly	Tyr	Glu
				245					250					255	
Asp	Glu	Glu	Arg	Ser	Arg	Leu	Leu	Leu	Val	Glu	Gly	Ser	Ile	Ala	Glu
			260					265					270		
Lys	Trp	Lys	Asp	Arg	Leu	Gly	Lys	Lys	Val	Lys	Arg	Trp	Asp	Met	Lys
			275				280					285			
Leu	Arg	His	Leu	Gly	Leu	Ser	Asp	Ser	Ser	Ser	Asp	Ser	Thr	Gln	Ser
			290				295					300			
Gln	Lys	Pro	Gly	Arg	Asn	Ser	Asn	Ser	Arg	Gln	Ala	Arg	Asn		
305					310					315					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu	Thr	Val	Asn	Leu	Tyr	Thr	Ser	Ala	Gly	Cys	Leu	Cys	Pro	Pro	Leu
1				5					10				15		
Asn	Val	Asn	Glu	Glu	Tyr	Leu	Ile	Met	Gly	Tyr	Glu	Phe	Pro		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GARACHG TSA AYCTBTAYAC N

21

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RAAYTCRTAN CCCATNAT

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 13...13
- (D) OTHER INFORMATION: Aspartic Acid or Histidin
e

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Xaa Gly Ala Asp
1 5 10 15
Phe Pro Met

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Gly Cys Glu Pro Ile Leu Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gly Cys Glu Pro Ile Leu Ile Cys Ala Trp Pro Pro Leu Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Thr Val Asn Leu Tyr Thr Ser Ala Gly Cys Leu Cys Pro Pro Leu
1 5 10 15
Asn Val Asn Glu Tyr Leu Ile Met Gly Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Val Asn Leu Tyr Thr Ser Ser Gly Cys Leu Cys Pro Pro Leu
1 5 10 15
Asn Val Asn Glu Tyr Leu Ile Met Gly Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTCTGGCTG CCTGTGTCCT CCACTTAACG

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTCCACTTA ACGTTAATGA GGAGTATCTC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGGAACATGA CTAAGATGCC C

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATATACTGG CAGCTCCTCG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTTTTGGG AAGCCTTCAT GG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCATCGTGGC ATTTCACTTT CA

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTACTGTGC CAGTCTTCCC TGTAACCAGC GACCTGTATT CCCCCAAGTA AGCCTACACA 60
TACAGGTTGG GCAGAATAAC AATGTCTCCA ACAAGGAAAT TGGACTCATT CCTGCTACTG 120
GTCATACCTG GACTGGTGCT TCTCTTATTA CCAATGCTT ACTGTGCTTC GTGTGAGCCT 180
GTGCGGATTC CCATGTGCAA ATCTATGCCA TGGAACATGA CCAAGATGCC CAACCATCTC 240
CACCACAGCA CTCAGGCCAA TGCTATCCTG GCAATTGAAC AGTTTGAAGG TTTGCTGACC 300
TACTGAATGTA GCCAGGACCT TTTGTCTTT CTGTGTGCCA TGTATGCCCC CATTGTACC 360
ATCGATTTC AGCATGAACC AATTAAAGCT TGCAAGTCCG TGTGCGAAAG GGCCAGGGCC 420
GGCTGTGAGC CCATTCTCAT AAAGTACCGG CACACTTGGC CAGAGAGCT GGCATGTGAA 480
GAGCTGCCCG TATATGACAG AGGAGTCTGC ATCTCCCGAG AGGCTATCGT CACAGTGGAA 540
CAAGGAACAG ATTCAATGCC AGACTTCCCC ATGGATTCAA ACAATGGAAA TTGCGGAAGC 600
ACGGCAGGTG AGCACTGTAA ATGCAAGCCC ATGAAGGCTT CCAAAAAGAC GTATCTCAAG 660
AATAATTACA ATTATGTAAT CAGAGCAAAA GTGAAAGAGG TGAAGTGAA ATGCCACGAC 720
GCAACAGCAA TTGTGGAAGT AAAGGAGATT CTCAGTCTT CCCTAGTGAA CATTCTCTAAA 780
GACACAGTGA CACTGTACAC CAACTCAGGC TGCTTGTGCC CCCAGCTTGT TGCCAATGAG 840
GAATACATAA TTATGGGCTA TGAAGACAAA GAGCGTACCA GGCTTCTACT AGTGGGAAGGA 900
TCCTTGGCCG AAAAATGGAG AGATCGTCTT GCTAAGAAAG TCAAGCGCTG GGATCAAAAG 960
CTTCGAGCTC CCAGGAAAAG CAAAGACCCC GTGGCTCCAA TTCCCAACAA AAACAGCAAT 1020
TTCAGACAAG CGCGTAGTTA GACTAACGGA AAGGTGTATG GAACTCTAT GGACTTTGAA 1080
ACTAAGATTT GCATTGTGG AAGAGCAAAA AAGAAATTC ACTACAGAC GTTATATCT 1140
ATTGTTTACT ACAAGAGCT GGTTTAGTTG ATTGTAGTTC TCCTTCTCTT CTTTCTTTTA 1200
TAACATATATT GCACGTGTTT CAGGCAGTTT ATCAACTTCC AGTGACAGAG CAGTGACTGA 1260
ATGTAGCTAA GAGCCTATCA TCTGATCACT A 1291